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Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=3; day=10; hr=11; min=50; sec=17; ms=172;]

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Application No: 10580906 Version No: 1.0

Input Set:**Output Set:**

Started: 2008-03-10 09:47:19.337
Finished: 2008-03-10 09:47:24.762
Elapsed: 0 hr(s) 0 min(s) 5 sec(s) 425 ms
Total Warnings: 20
Total Errors: 14
No. of SeqIDs Defined: 20
Actual SeqID Count: 20

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
W 402	Undefined organism found in <213> in SEQ ID (2)
W 402	Undefined organism found in <213> in SEQ ID (3)
W 402	Undefined organism found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (7)
W 402	Undefined organism found in <213> in SEQ ID (8)
W 402	Undefined organism found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)

Input Set:

Output Set:

Started: 2008-03-10 09:47:19.337
Finished: 2008-03-10 09:47:24.762
Elapsed: 0 hr(s) 0 min(s) 5 sec(s) 425 ms
Total Warnings: 20
Total Errors: 14
No. of SeqIDs Defined: 20
Actual SeqID Count: 20

Error code	Error Description
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (20)

SEQUENCE LISTING

<110> FUKATSU et al.

<120> RECEPTOR FUNCTION REGULATING AGENT

<130> 20039.0005USWO

<140> 10580906

<141> 2008-03-10

<150> PCT/JP2004/017996

<151> 2004-11-26

<150> JP 2003-394848

<151> 2003-11-26

<160> 20

<170> PatentIn Version 3.1

<210> 1

<211> 361

<212> PRT

<213> Human

<400> 1

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Leu Glu Gln Ala Asn Arg Thr Arg Phe Pro Phe Phe Ser Asp Val Lys
      20              25              30
Gly Asp His Arg Leu Val Leu Ala Ala Val Glu Thr Thr Val Leu Val
      35              40              45
Leu Ile Phe Ala Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu
      50              55              60
Val Ala Arg Arg Arg Arg Arg Gly Ala Thr Ala Cys Leu Val Leu Asn
      65              70              75              80
Leu Phe Cys Ala Asp Leu Leu Phe Ile Ser Ala Ile Pro Leu Val Leu
      85              90              95
Ala Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Ala Cys His
      100             105             110
Leu Leu Phe Tyr Val Met Thr Leu Ser Gly Ser Val Thr Ile Leu Thr
      115             120             125
Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile Val His Leu Gln
      130             135             140
Arg Gly Val Arg Gly Pro Gly Arg Arg Ala Arg Ala Val Leu Leu Ala
      145             150             155             160
Leu Ile Trp Gly Tyr Ser Ala Val Ala Ala Leu Pro Leu Cys Val Phe
      165             170             175
Phe Arg Val Val Pro Gln Arg Leu Pro Gly Ala Asp Gln Glu Ile Ser
      180             185             190
Ile Cys Thr Leu Ile Trp Pro Thr Ile Pro Gly Glu Ile Ser Trp Asp
      195             200             205
Val Ser Phe Val Thr Leu Asn Phe Leu Val Pro Gly Leu Val Ile Val
      210             215             220
Ile Ser Tyr Ser Lys Ile Leu Gln Ile Thr Lys Ala Ser Arg Lys Arg

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225		230		235		240
Leu Thr Val Ser	Leu Ala Tyr Ser	Glu Ser His Gln	Ile Arg Val Ser			
	245	250	255			
Gln Gln Asp Phe	Arg Leu Phe Arg	Thr Leu Phe Leu	Leu Met Val Ser			
	260	265	270			
Phe Phe Ile Met	Trp Ser Pro Ile	Ile Thr Ile Leu	Leu Ile Leu			
	275	280	285			
Ile Gln Asn Phe	Lys Gln Asp Leu	Val Ile Trp Pro	Ser Leu Phe Phe			
	290	295	300			
Trp Val Val Ala	Phe Thr Phe Ala	Asn Ser Ala Leu	Asn Pro Ile Leu			
305	310	315	320			
Tyr Asn Met Thr	Leu Cys Arg Asn	Glu Trp Lys Lys	Ile Phe Cys Cys			
	325	330	335			
Phe Trp Phe Pro	Glu Lys Gly Ala	Ile Leu Thr Asp	Thr Ser Val Lys			
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Arg Asn Asp Leu	Ser Ile Ile Ser	Gly				
	355	360				

<210> 2

<211> 1083

<212> DNA

<213> Human

<400> 2

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gcggtggaga	caaccgtgct	ggtgctcatc	tttgcaagtgt	cgctgctggg	caacgtgtgc	180
gccctggtgc	tgggtggcgcg	ccgacgacgc	cgcggcgcga	ctgcctgcct	ggtactcaac	240
ctcttctgcg	cggacctgct	cttcatcagc	gctatccctc	tgggtgctggc	cgtgcgctgg	300
actgaggcct	ggctgctggg	ccccgttgcc	tgccacctgc	tcttctacgt	gatgaccctg	360
agcggcagcg	tcaccatcct	cacgctggcc	gcggtcagcc	tggagcgcct	ggtgtgcatc	420
gtgcacctgc	agcgcggcgt	gcggggctct	ggcggcgggg	cgcgggcagt	gctgctggcg	480
ctcatctggg	getattcggc	ggtegccgct	ctgcctctct	gcgtcttctt	ccgagtcgtc	540
ccgcaacggc	tccccggcgc	cgaccaggaa	atttcgattt	gcacactgat	ttggcccacc	600
attcctggag	agatctcgtg	ggatgtctct	tttgttactt	tgaacttctt	ggtgccagga	660
ctggtcattg	tgatcagtta	ctccaaaatt	ttacagatca	caaaggcatc	aaggaagagg	720
ctcacggtaa	gcctggccta	ctcgagagac	caccagatcc	gcgtgtccca	gcaggacttc	780
cggctcttcc	gcacctctct	cctcctcatg	gtctccttct	tcatcatgtg	gagccccatc	840
atcatcacca	tctcctcat	cctgatccag	aacttcaagc	aagacctggg	catctggccg	900
tcctcttctt	tctgggtggg	ggccttcaca	tttgctaatt	cagccctaaa	ccccatcctc	960
tacaacatga	cactgtgcag	gaatgagtgg	aagaaaattt	tttgctgctt	ctgggtccca	1020
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ggc						1083

<210> 3

<211> 361

<212> PRT

<213> Mouse

<400> 3

Met Ser Pro Glu	Cys Ala Gln Thr	Thr Gly Pro Gly	Pro Ser His Thr
	5	10	15
Leu Asp Gln Val	Asn Arg Thr His	Phe Pro Phe Phe	Ser Asp Val Lys
	20	25	30
Gly Asp His Arg	Leu Val Leu Ser	Val Val Glu Thr	Thr Val Leu Gly
	35	40	45
Leu Ile Phe Val	Val Ser Leu Leu	Gly Asn Val Cys	Ala Leu Val Leu

50	55	60
Val Ala Arg Arg Arg Arg Arg Gly Ala Thr Ala Ser Leu Val Leu Asn		
65	70	75 80
Leu Phe Cys Ala Asp Leu Leu Phe Thr Ser Ala Ile Pro Leu Val Leu		
	85	90 95
Val Val Arg Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Val Cys His		
	100	105 110
Leu Leu Phe Tyr Val Met Thr Met Ser Gly Ser Val Thr Ile Leu Thr		
	115	120 125
Leu Ala Ala Val Ser Leu Glu Arg Met Val Cys Ile Val Arg Leu Arg		
	130	135 140
Arg Gly Leu Ser Gly Pro Gly Arg Arg Thr Gln Ala Ala Leu Leu Ala		
	145	150 155 160
Phe Ile Trp Gly Tyr Ser Ala Leu Ala Ala Leu Pro Leu Cys Ile Leu		
	165	170 175
Phe Arg Val Val Pro Gln Arg Leu Pro Gly Gly Asp Gln Glu Ile Pro		
	180	185 190
Ile Cys Thr Leu Asp Trp Pro Asn Arg Ile Gly Glu Ile Ser Trp Asp		
	195	200 205
Val Phe Phe Val Thr Leu Asn Phe Leu Val Pro Gly Leu Val Ile Val		
	210	215 220
Ile Ser Tyr Ser Lys Ile Leu Gln Ile Thr Lys Ala Ser Arg Lys Arg		
	225	230 235 240
Leu Thr Leu Ser Leu Ala Tyr Ser Glu Ser His Gln Ile Arg Val Ser		
	245	250 255
Gln Gln Asp Tyr Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser		
	260	265 270
Phe Phe Ile Met Trp Ser Pro Ile Ile Ile Thr Ile Leu Leu Ile Leu		
	275	280 285
Ile Gln Asn Phe Arg Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe		
	290	295 300
Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu		
	305	310 315 320
Tyr Asn Met Ser Leu Phe Arg Asn Glu Trp Arg Lys Ile Phe Cys Cys		
	325	330 335
Phe Phe Phe Pro Glu Lys Gly Ala Ile Phe Thr Asp Thr Ser Val Arg		
	340	345 350
Arg Asn Asp Leu Ser Val Ile Ser Ser		
	355	360

<210> 4
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 <212> DNA
 <213> Mouse

<400> 4

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gtcgtggaga ccaccgttct ggggctcatc tttgtcgtct cactgctggg caacgtgtgt	180
gctctagtgc tgggtggcgcg ccgtcggcgc cgtggggcga cagccagcct ggtgctcaac	240
ctcttctgcg cggatttgct cttcaccagc gccatccctc tagtgctcgt cgtgcgctgg	300
actgaggcct ggctgttggg gcccgctcgc tgccacctgc tcttctacgt gatgacaatg	360
agcggcagcg tcacgatact cacactggcc gcggtcagcc tggagcgcac ggtgtgcatc	420
gtgcgcctcc ggcgcggcct gagcggcccg ggcggcgga ctcaggcggc actgctggct	480
ttcatatggg gttactcggc gctcgcgcgc ctgcccctct gcatcttggt ccgcgtggtc	540
ccgcagcgc ttcccggcgg ggaccaggaa attccgattt gcacattgga ttggcccaac	600
cgcataggag aaatctcatg ggatgtgttt tttgtgactt tgaacttcct ggtgccggga	660

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ctggtcattg tgatcagtta ctccaaaatt ttacagatca cgaaagcatc gcggaagagg 720
cttacgctga gcttggcata ctctgagagc caccagatcc gagtgtccca acaagactac 780
cgactcttcc gcacgctctt cctgctcatg gtttccttct tcatcatgtg gagtcccac 840
atcatcacca tcctcctcat cttgatccaa aacttcgggc aggacctggt catctggcca 900
tcctttttct tctgggtggt ggccttcacg tttgccaaact ctgccctaaa ccccatactg 960
tacaacatgt cgctgttcag gaacgaatgg aggaagattt tttgctgctt cttttttcca 1020
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agc 1083

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<210> 5
<211> 20
<212> DNA
<213> Artificial Sequence

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<220>
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<222> (1)..(20)
<223> primer

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<400> 5
gctgtggcat gcttttaaac 20

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<210> 6
<211> 20
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<220>
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<400> 6
cgctgtggat gtctatttgc 20

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<210> 7
<211> 30
<212> DNA
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<220>
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<223> probe

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<400> 7
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<210> 8
<211> 361
<212> PRT
<213> Rat

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<400> 8
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      5              10              15
Pro Asp Gln Val Asn Arg Thr His Phe Pro Phe Phe Ser Asp Val Lys

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ccgcagcgcc	ttcccgcg	ggaccaggaa	attccgattt	gcacattgga	ttggcccaac	600
cgcataggag	aaatctcatg	ggatgtgttt	tttgtgactt	tgaacttcct	ggtaccagga	660
ctggtcattg	tgatcagcta	ctccaagatt	ttacagatca	cgaaagcctc	gcggaagagg	720
cttacgctga	gcttggcata	ctccgagagc	caccagatcc	gagtgtccca	gcaggactac	780
cggctcttcc	gaacgctctt	cctgctcatg	gtttccttct	tcattcatgtg	gagtcccatc	840
atcatcacca	tcctcctcat	cttgatccag	aacttcgggc	aggacctggt	tatctggccg	900
tcctttttct	tctgggtggt	ggccttcacg	tttgccaaact	ccgcctaaa	ccccattctg	960
tacaacatgt	cgtgttccag	gagcgagtgg	aggaagattt	tttgcctgctt	ctttttccca	1020
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acc						1083

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<210> 12
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 <222> (1)..(26)
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<220>
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<222> (1)..(33)
<223> primer

<400> 13
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<210> 14
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<220>
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<222> (1)..(33)
<223> primer

<400> 14
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<220>
<221> misc_feature
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<223> primer

<400> 15
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<210> 16
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<220>
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<222> (1)..(24)
<223> primer

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<223> probe

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<210> 18
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<400> 19
cgctcctgaa cagcgacat 19

<210> 20
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<213> Artificial Sequence

<220>
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<222> (1)..(26)
<223> probe

<400> 20
caactccgcc ctaaacccca ttctgt 26